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Tropical fungal diversity: closing the gap between species estimates and species discovery

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The collection of papers in this special issue examines the nature of some of the ecosystem and environmental interactions involving fungi in the tropics and the biodiversity of certain of these tropical fungal guilds in an effort to provide improved estimates to answer the question of just how much undescribed tropical fungal diversity remains to be discovered. Fungi are ubiquitously found in all tropical environments where they are essential for ecosystem processes. For example, in interactions with plants, fungi facilitate nutrient uptake (as mycorrhizas), provide protection against phytopathogens (as endophytes, phylloplane constituents or mycoparasites), breakdown and recycle the nutrients otherwise locked in cell wall compounds (as wood and litter decomposers), and act as agents of disease. They cover a broad range of life forms and life histories from microscopic yeasts to those having large and conspicuous sporocarps or genets covering many hectares. Tropical regions are incredibly species rich, harbouring the majority of terrestrial biodiversity as well as a broad variety of often unusual interactions between species. Yet despite increasing interest, our understanding of the mycobiota and its roles in tropical ecosystems is woefully incomplete.

The question of how many fungal species there are is indisputably important. Current estimates of these numbers range from 611,000 (Mora et al. 2011) to nearly ten million (Cannon 1997). However, Hawksworth's (1991) estimate of 1.5 million species remains, for most, the benchmark. One of the several caveats of the Hawksworth (1991) study was the dearth of information with regard to fungal biodiversity within tropical ecosystems and the lack of data from which we could reliably extrapolate tropical species numbers. Nonetheless, the structural complexity of tropical forests combined with the diversity of niches and warm, moist climates make it a near certainty that large numbers, if not the majority, of undescribed fungal species reside in the tropics (Hawksworth 1993) as has been determined for some vertebrate groups (Giam et al. 2012).

Difficulties in estimating fungal species diversity at any given site abound. Fungal communities are highly diverse and, due to their cryptic and often ephemeral nature, the probability of encountering and recording all species present during any sampling effort is low. Indeed, because of the issues associated with fully enumerating a fungal community, many of the studies in this special issue use species richness estimators of one kind or another. However, until recently, lack of

long-term fungal datasets in tropical sites has hindered our ability to begin to estimate how well our sampling efforts may be at capturing the full complement of fungal species richness. The studies by Piepenbring et al. (2012) and Henkel et al. (2012) are important as they provide data on species accumulation rates after repeated samplings. Piepenbring et al. (2012) show how species accumulation curves for plants in a small area in Panama saturated fairly rapidly during sampling (24 visits over two years in total) but the associated fungal community did not reach an asymptote. Henkel et al. (2012) examined plots in Guyana over seven years for ectomycorrhizal macrofungi. One of the most interesting results from their study is that the species accumulation curve appears to have flattened, but when compared with the study of Smith et al. (2011) who examined ectomycorrhizas on the roots of three legume trees, only 40 % of the fungi found as ectomycorrhizas had been discovered as sporocarps during the seven-year sampling period. This indicates that many species remain to be found that have not yet been sampled as sporocarps and reinforces the ephemeral nature of their formation.

Likewise, determining the factors that affect species diversity and community composition across scales is still an open question. López-Quintero et al. (2012) examine the changes in fungal composition between forest types. First, they examine forests at various stages of recovery following agricultural clearance and secondly they determine the compositional change between two sites in the Colombian Amazon. In their study, fungal diversity did not necessarily increase with secondary forest age (as is commonly shown for trees, e.g. Letcher & Chazdon 2009) and, in addition, they showed a high turnover in species composition between their two study sites. Gómez-Hernández et al. (2012) present data showing that fungi from an elevational transect in Mexico exhibit a mid-elevation peak in species richness as found in many other plant and animal taxa (Rahbek 1995), but that the patterns are somewhat different for xylophagous and ectomycorrhizal fungi.

Many fungi are cryptic sporocarp producers, and, when they are found, are difficult to identify morphologically. For this and other reasons, molecular tools have been particularly valuable in fungal ecology/diversity studies that strive to document or analyze fungal communities. However, when using molecular identifications it is important to be able to consistently delineate molecular operational taxonomic units (analogous to species) across different studies and/or different loci. The study of Setaro et al. (2012) is important in that it sets out to optimize distance thresholds for the two most commonly used loci (ITS and LSU) to maximize comparability of sequence data generated by different studies. Then data generated from *Sebacinales* species sampled as mycorrhizae in tropical (Ecuador) and temperate regions are compared to determine that these fungi may be equally diverse in both regions. Phosri et al.'s molecular study (2012) on ectomycorrhizal fungi in a tropical dry forest in Thailand showed a moderate to low diversity of fungi on tree roots and a fungal community with similarities to both temperate and tropical biomes. These, and other papers in this issue, may assist in the current debate as to whether a 'reverse latitudinal gradient' exists for mycorrhizal fungi (Tedersoo & Nara 2010).

The Hawksworth (1991) estimate was established based on a ratio of plant:fungal species in temperate regions. Whether these ratios hold up in tropical regions is indirectly assessed in the papers of Berndt (2012) and Mangelsdorff et al. (2012) with sometimes conflicting results, highlighting the value of both sound taxonomic and monographic treatments as well as the need for more long term fungal studies in tropical regions. For instance, the rust fungi (obligate plant pathogens) may be the best documented group of microfungi, yet Berndt (2012) found that ratios of known plant:rust species in Neotropical countries ranged from 1:16 to 1:124 – no doubt a reflection, at least in part, of undersampling for fungi in most of these areas.

Lücking (2012) asks the question of not just how many species remain to be discovered, but of what form these species may take. He uses a novel 'character correlation index' whereby combinations of traits that are known to be correlated in currently described species are used to predict the traits that are expected to be correlated and found in currently unknown species. He predicts that another 48 lichen-forming fungi in the *Graphis* group alone remain to be discovered, approximately doubling the known number in this genus.

The impacts of disturbances on fungal communities have been poorly studied in tropical regions, perhaps because these communities have been considered, likely wrongly, as both resistant and resilient to disturbance (Allison & Martiney 2009). Three papers in this issue address this assumption: da Silva et al. (2012) determine the impact of mining and restoration in Brazilian restinga on communities of arbuscular mycorrhizal fungi by counting and identifying spores. Hattori et al. (2012) show how diversity of polypore fungi is dependent upon the presence of suitable host trees that may be removed by logging or conversion to plantations in their Malaysian study sites. And, as already discussed, López-Quintero et al (2012) examine the effects of clearance for shifting cultivation and subsequent forest recovery on fungal diversity.

Just as the study of Berndt (2012) shows that species data is unevenly distributed geographically, other papers in this issue show that there are, likewise, a number of specialized habitats that still remain to be fully assessed for tropical fungal diversity. These include fungi inhabiting insect guts, among which are the Trichomycetes that have been reviewed by Lichtwardt (2012). The abundance and diversity of insect host species will clearly affect fungal species diversity and an improved assessment of insect-associated fungal diversity in the tropics is certainly a priority for mycologists. Finally, Jones and Pang (2012) provide a timely review of tropical aquatic fungi, highlighting areas in need of future research.

Hawksworth (2012) completes this special issue with a re-examination of the 1.5 million fungal species estimate taking into consideration new studies from the tropics and the increasing number of molecular diversity studies published since his original estimate. This rounds out these contributions that we hope will help us move towards a better understanding of fungal diversity in the tropics.

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